

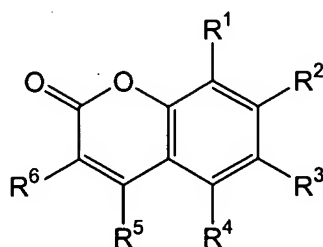
Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1-83 (canceled)

84 (new): A material having a fluorogenic moiety linked to a solid support, said material having the structure:



wherein:

R¹, R³, R⁴ and R⁶ are each H;

R² is -NHR¹⁵; and

R⁵ is -R¹⁴-SS,

wherein:

R¹⁴ is -CH₂C(O)NH-;

R¹⁵ is a member selected from the group consisting of amine protecting groups, -C(O)-AA and -C(O)-P:

wherein:

P is a peptide sequence;

AA is an amino acid residue; and

SS is a solid support.

1 **85** (new): The material in accordance with claim **84**, wherein R¹⁵ is an amine
2 protecting group.

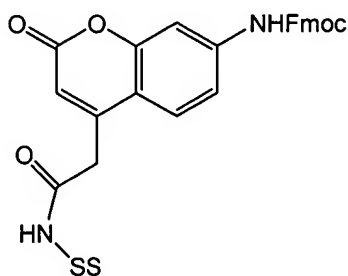
1 **86** (new): The material in accordance with claim **85**, wherein said amine
2 protecting group is 9-fluorenylmethoxycarbonyl (Fmoc).

1 **87** (new): The material in accordance with claim **84**, wherein R¹⁵ is -C(O)-AA,
2 wherein AA is an amino acid residue.

1 **88** (new): The material in accordance with claim **84**, wherein R¹⁵ is -C(O)-P,
2 wherein P is a peptide sequence.

1 **89** (new): The material in accordance with claim **84**, wherein the solid support is
2 a Rink resin.

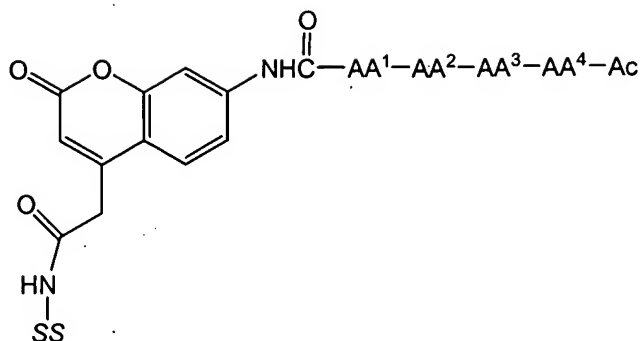
1 **90** (new): A material having a fluorogenic moiety linked to a solid support, said
2 material having the structure:



3
wherein:

4 SS is a solid support, wherein said the support is a Rink resin.

1 **91** (new): A library of fluorogenic peptides comprising sub-libraries P1, P2, P3
2 and P4, wherein each of the sub-libraries P1, P2, P3 and P4 comprises tetrapeptides having the
3 structure:



wherein:

SS is a solid support, and

wherein:

for sub-library P1, each AA¹ is a different amino acid of the 20 amino acids, and each of AA²-AA⁴ is an isokinetic mixture of 20 amino acids;

for sub-library P2, each of AA² is a different amino acid of the 20 amino acids, and each of AA¹, AA³ and AA⁴ is an isokinetic mixture of 20 amino acids;

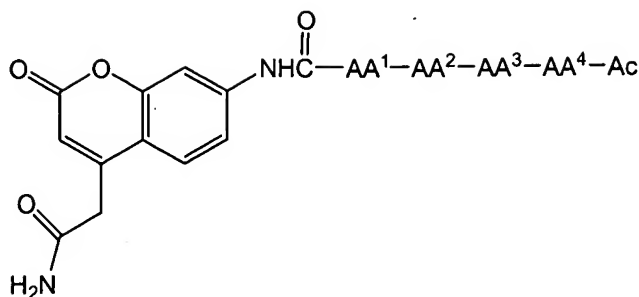
for sub-library P3, each of AA³ is a different amino acid of the 20 amino acids, and each of AA¹, AA² and AA⁴ is an isokinetic mixture of 20 amino acids; and

for sub-library P4, each of AA⁴ is a different amino acid of the 20 amino acids, and each of AA¹, AA² and AA³ is an isokinetic mixture of 20 amino acids.

92 (new): The library in accordance with claim 91, wherein the 20 amino acids are the 20 naturally occurring amino acids excluding cysteine and including norleucine.

93 (new): The library in accordance with claim 91, wherein the solid support is a Rink resin.

94 (new): A library of fluorogenic peptides comprising sub-libraries P1, P2, P3 and P4, wherein each of the sub-libraries P1, P2, P3 and P4 comprises tetrapeptides having the structure:



wherein:

for sub-library P1, each AA^1 is a different amino acid of the 20 amino acids, and each of AA^2 - AA^4 is an isokinetic mixture of 20 amino acids;

for sub-library P2, each of AA^2 is a different amino acid of the 20 amino acids, and each of AA^1 , AA^3 and AA^4 is an isokinetic mixture of 20 amino acids;

for sub-library P3, each of AA^3 is a different amino acid of the 20 amino acids, and each of AA^1 , AA^2 and AA^4 is an isokinetic mixture of 20 amino acids; and

for sub-library P4, each of AA^4 is a different amino acid of the 20 amino acids, and each of AA^1 , AA^2 and AA^3 is an isokinetic mixture of 20 amino acids.

95 (new): The library in accordance with claim 94, wherein the 20 amino acids are the 20 naturally occurring amino acids excluding cysteine and including norleucine.

96 (new): A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising:

(a) contacting said protease with a library of peptides according to claim 91 or claim 94 in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;

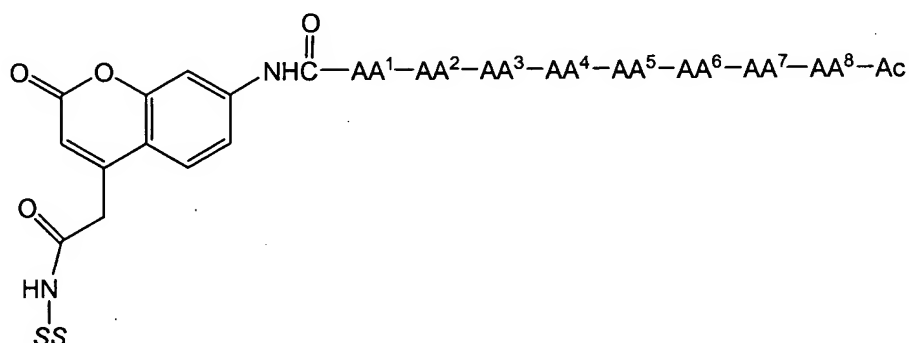
(b) detecting said fluorescent moiety;

(c) determining the sequence of said peptide sequence, thereby determining said peptide sequence specificity profile of said protease.

1 **97** (new): The method according to claim **96**, further comprising (d) quantifying
2 said fluorescent moiety, thereby quantifying said protease.

1 **98** (new): The method according to claim **97**, wherein said protease is a member
2 selected from the group consisting of aspartic protease, cysteine protease, metalloprotease and
3 serine protease.

1 **99** (new): A library of fluorogenic peptides comprising sub-libraries P1, P2, P3
2 and P4, wherein each of the sub-libraries P1, P2, P3 and P4 comprises hexapeptides having the
3 structure:



4
5 wherein:

6 SS is a solid support, and

7 wherein:

8 for each sub-library P1, P2, P3 and P4, AA¹, AA², AA³ and AA⁴ in each of the
9 hexapeptides are the same amino acid residues;

10 for sub-library P1, each of AA⁵ is a different amino acid of the 20 amino acids,
11 and each of AA⁶, AA⁷ and AA⁸ is an isokinetic mixture of 20 amino acids;

12 for sub-library P2, each of AA⁶ is a different amino acid of the 20 amino acids,
13 and each of AA⁵, AA⁷ and AA⁸ is an isokinetic mixture of 20 amino acids;

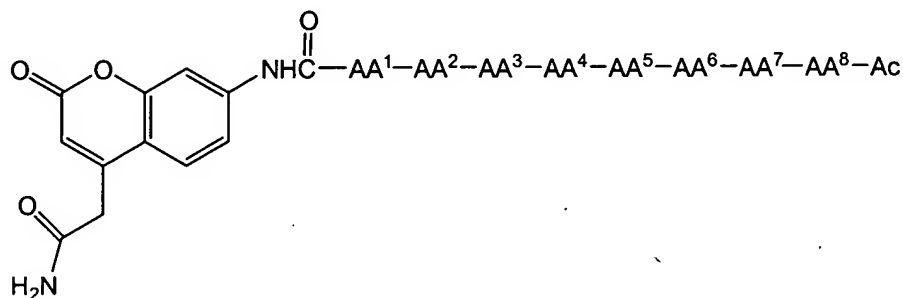
14 for sub-library P3, each of AA⁷ is a different amino acid of the 20 amino acids,
15 and each of AA⁵, AA⁶ and AA⁸ is an isokinetic mixture of 20 amino acids; and

for sub-library P4, each of AA⁸ is a different amino acid of the 20 amino acids,
and each of AA⁵, AA⁶ and AA⁷ is an isokinetic mixture of 20 amino acids.

100 (new): The library in accordance with claim 99, wherein the 20 amino acids
are the 20 naturally occurring amino acids excluding cysteine and including norleucine.

101 (new): The library in accordance with claim 99, wherein the solid support is
a Rink resin.

102 (new): A library of fluorogenic peptides comprising sub-libraries P1, P2, P3
and P4, wherein each of the sub-libraries P1, P2, P3 and P4 comprises hexapeptides having the
structure:



wherein:

for each sub-library P1, P2, P3 and P4, AA¹, AA², AA³ and AA⁴ in each of the
hexapeptides are the same amino acid residues;

for sub-library P1, each of AA⁵ is a different amino acid of the 20 amino acids,
and each of AA⁶, AA⁷ and AA⁸ is an isokinetic mixture of 20 amino acids;

for sub-library P2, each of AA⁶ is a different amino acid of the 20 amino acids,
and each of AA⁵, AA⁷ and AA⁸ is an isokinetic mixture of 20 amino acids;

for sub-library P3, each of AA⁷ is a different amino acid of the 20 amino acids,
and each of AA⁵, AA⁶ and AA⁸ is an isokinetic mixture of 20 amino acids; and

for sub-library P4, each of AA⁸ is a different amino acid of the 20 amino acids,
and each of AA⁵, AA⁶ and AA⁷ is an isokinetic mixture of 20 amino acids.

1 **103 (new):** The library in accordance with claim **102**, wherein the 20 amino
2 acids are the 20 naturally occurring amino acids excluding cysteine and including norleucine.

1 **104 (new):** A method of determining a peptide sequence specificity profile of an
2 enzymatically active protease, said method comprising:

3 (a) contacting said protease with a library of peptides according to claim **99** or
4 claim **102** in such a manner whereby the fluorogenic moiety is released
5 from the peptide sequence, thereby forming a fluorescent moiety;

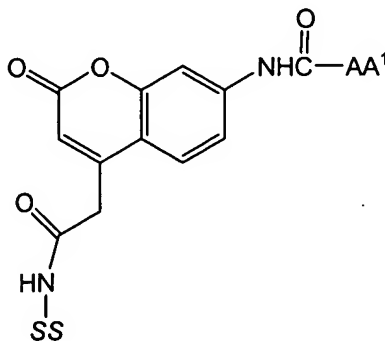
6 (b) detecting said fluorescent moiety;

7 (c) determining the sequence of said peptide sequence, thereby determining said
8 peptide sequence specificity profile of said protease.

1 **105 (new):** The method according to claim **104**, further comprising (d)
2 quantifying said fluorescent moiety, thereby quantifying said protease.

1 **106 (new):** The method according to claim **105**, wherein said protease is a
2 member selected from the group consisting of aspartic protease, cysteine protease,
3 metalloprotease and serine protease.

1 **107 (new):** A library of twenty fluorogenic amino acid amides having the
2 structure:



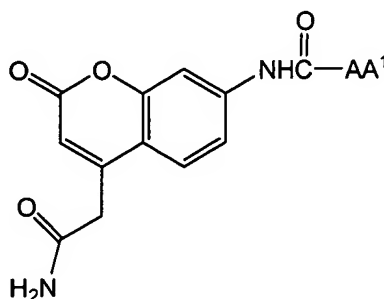
3
4 wherein:

5 *SS* is a solid support, and
6 each AA¹ for the twenty fluorogenic amino acid amides is a different amino acid
7 residue.

1 **108** (new): The library in accordance with claim **107**, wherein the amino acid
2 residues are the 20 naturally occurring amino acids excluding cysteine and including norleucine.

1 **109** (new): The library in accordance with claim **108**, wherein the solid support
2 is a Rink resin.

1 **110** (new): A library of twenty fluorogenic amino acids having the structure:



2
3 wherein:

4 each AA¹ for the twenty fluorogenic amino acids is a different amino acid residue

1 **111** (new): The library in accordance with claim **110**, wherein the amino acid
2 residues are the 20 naturally occurring amino acids excluding cysteine and including norleucine..

1 **112** (new): A method of determining an amino acid specificity profile of an
2 enzymatically active protease, said method comprising:

3 (a) contacting said protease with a library of amino acids according to claim **108**
4 or claim **110** in such a manner whereby the fluorogenic moiety is released
5 from the amino acid, thereby forming a fluorescent moiety;

6 (b) detecting said fluorescent moiety;

7 (c) determining the identity of the amino acid, thereby determining said amino
8 acid specificity profile of said protease.

1 **113 (new):** The method according to claim **112**, further comprising (d)
2 quantifying said fluorescent moiety, thereby quantifying said protease.

1 **114 (new):** The method according to claim **113**, wherein said protease is a
2 member selected from the group consisting of aspartic protease, cysteine protease,
3 metalloprotease and serine protease.